Assign. 1 STA 445

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Directions:

This assignment covers chapter 5. Please show all work in this document and knit your final draft into a pdf. This is assignment is about statistical models, which will be helpful if you plan on taking STA 570, STA 371, or STA 571.

```
library(tidyverse)
```

Problem 1: Two Sample t-test

a. Load the `iris` dataset.

```
data('iris')
```

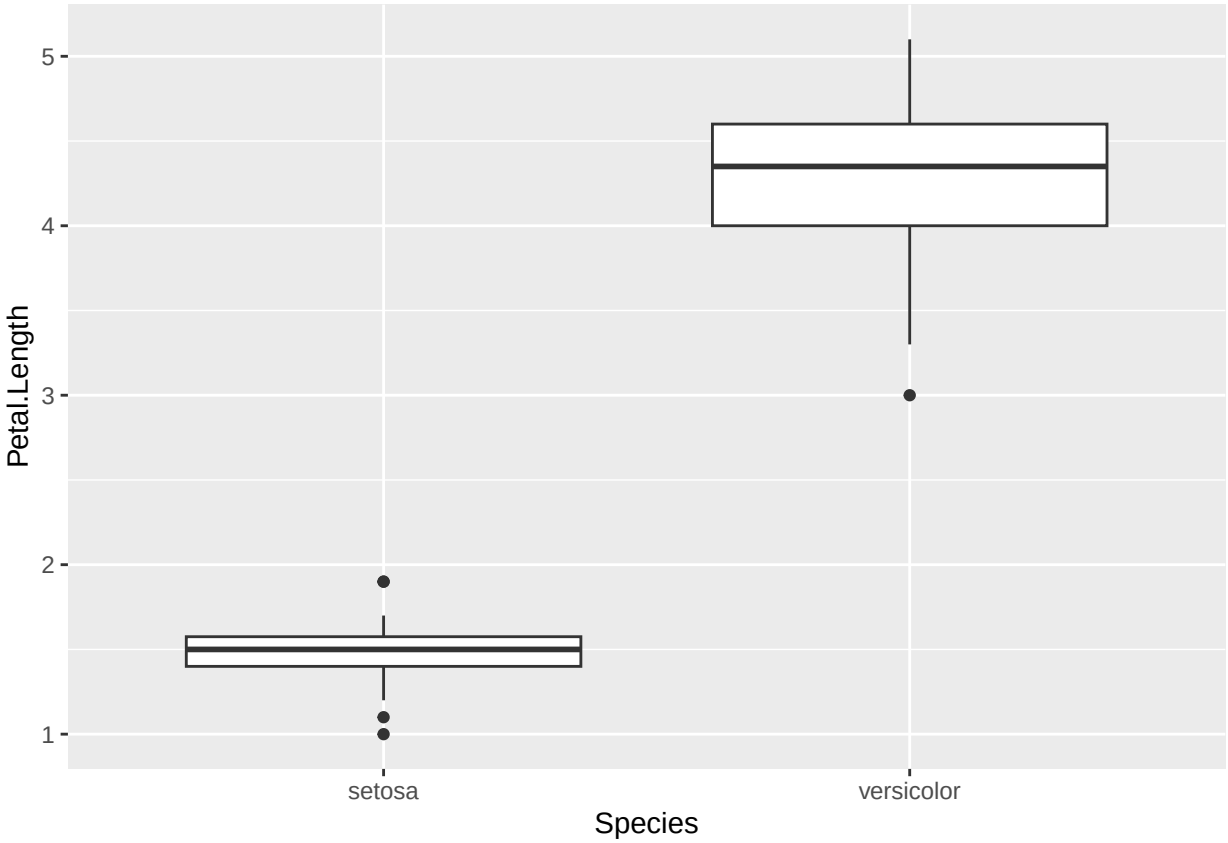
b. Create a subset of the data that just contains rows for the two species setosa and versicolor using filter. Use slice_sample to print out 20 random rows of the dataset.

```
iris1 <- iris %>%
  filter(Species=="setosa" | Species=="versicolor")
slice_sample(iris1)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.4         3.7          1.5         0.2  setosa
```

c. Create a box plot of the petal lengths for these two species using ggplot. Does it look like the mean petal length varies by species?

```
iris1 %>%
  ggplot(aes(x=Species, y=Petal.Length)) +
  geom_boxplot()
```



d. Do a two sample t-test using t.test to determine formally if the petal lengths differ. Note: The book uses the tidy function in the broom package to make the output "nice". I hate it! Please don't use tidy.

```
t.test(data=iris1, Petal.Length ~ Species)
```

```
##
##  Welch Two Sample t-test
##
## data:  Petal.Length by Species
## t = -39.493, df = 62.14, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group setosa and group versicolor is not eq
## 95 percent confidence interval:
##  -2.939618 -2.656382
## sample estimates:
##     mean in group setosa mean in group versicolor
##                    1.462                    4.260
```

d. What is the p-value for the test? What do you conclude?

P-value=2.2x10^-16

Since the p-value is very small, reject the null hypothesis.

There is significant evidence of a difference in mean petal length between setosa and versicolor flowers.

e. Give a 95% confidence interval for the difference in the mean petal lengths.

(-2.939618, -2.656382)

f. Give a 99% confidence interval for the difference in mean petal lengths. (Hint: type ?t.test. See that you can change the confidence level using the option conf.level)

```
t.test(data=iris1, Petal.Length ~ Species, conf.level=.99)
```

```
##
##  Welch Two Sample t-test
##
## data:  Petal.Length by Species
## t = -39.493, df = 62.14, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group setosa and group versicolor is not eq
## 99 percent confidence interval:
##  -2.986265 -2.609735
## sample estimates:
##     mean in group setosa mean in group versicolor
##                    1.462                    4.260
```

99% confidence level: (-2.986265, -2.609735)

g. What is the mean petal length for setosa?

1.462

h. What is the mean petal length for versicolor?

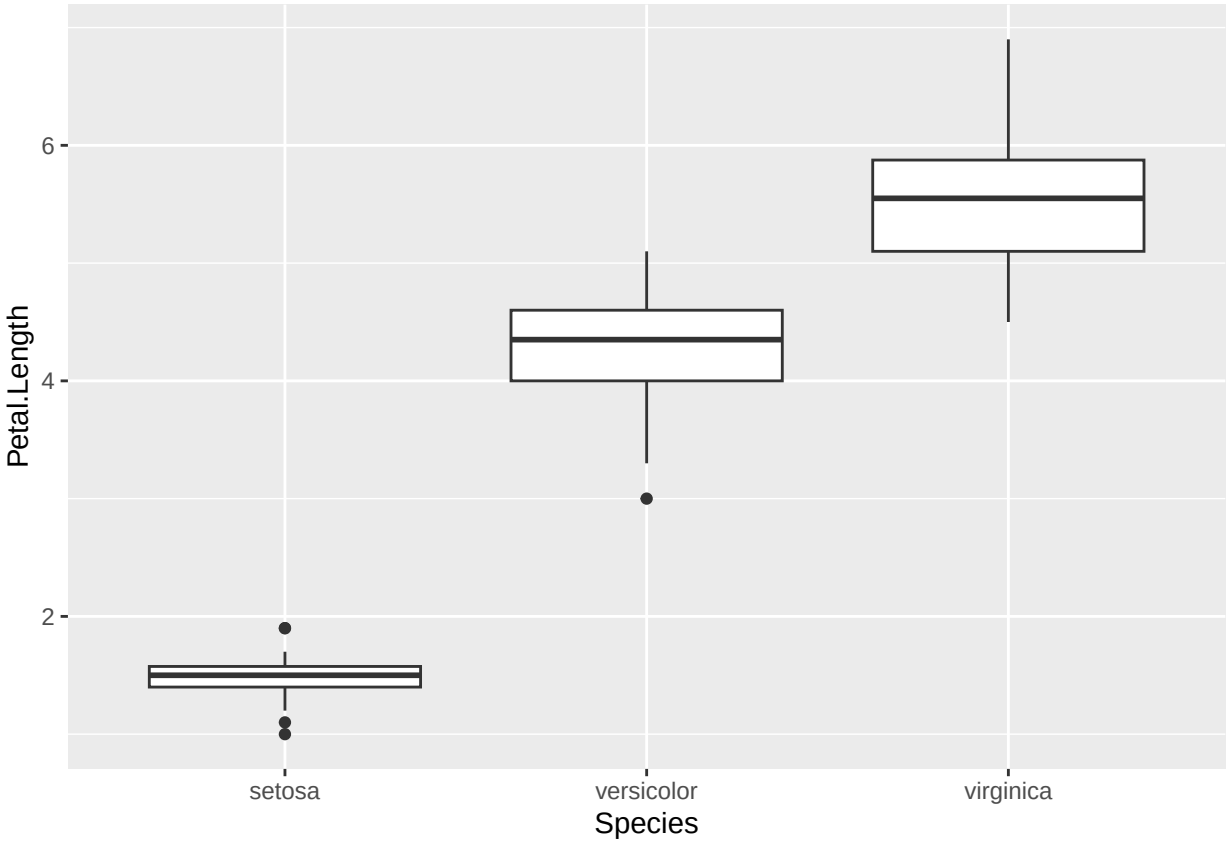
4.260

Problem 2: ANOVA

Use the iris data with all three species.

a. Create a box plot of the petal lengths for all three species using ggplot.Does it look like there are differences in the mean petal lengths?

```
iris %>%
  ggplot(aes(x=Species, y=Petal.Length)) +
  geom_boxplot()
```



b. Create a linear model where sepal length is modeled by species. Give it an appropriate name.

```
iris.model <- lm(data=iris, Sepal.Length ~ Species-1)
summary(iris.model)
```

```
##
## Call:
## lm(formula = Sepal.Length ~ Species - 1, data = iris)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.6880 -0.3285 -0.0060  0.3120  1.3120
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## Speciessetosa       5.0060     0.0728   68.76   <2e-16 ***
## Speciesversicolor   5.9360     0.0728   81.54   <2e-16 ***
## Speciesvirginica    6.5880     0.0728   90.49   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5148 on 147 degrees of freedom
## Multiple R-squared:  0.9925, Adjusted R-squared:  0.9924
## F-statistic:  6522 on 3 and 147 DF,  p-value: < 2.2e-16
```

c. Type anova(your model name) in a code chunk.

```
anova(iris.model)
```

```
## Analysis of Variance Table
##
## Response: Sepal.Length
##            Df Sum Sq Mean Sq F value    Pr(>F)
## Species     3 5184.9 1728.30  6521.7 < 2.2e-16 ***
## Residuals 147   39.0    0.27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

d. What is the p-value for the test? What do you conclude.

p-value= 2.2x10^-16.

Since p is very small, reject the null.

There is significant evidence that sepal length differs by species of flower.

e. Type summary(your model name) in a code chunk.

```
summary(iris.model)
```

```
##
## Call:
## lm(formula = Sepal.Length ~ Species - 1, data = iris)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.6880 -0.3285 -0.0060  0.3120  1.3120
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## Speciessetosa       5.0060     0.0728   68.76   <2e-16 ***
## Speciesversicolor   5.9360     0.0728   81.54   <2e-16 ***
## Speciesvirginica    6.5880     0.0728   90.49   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5148 on 147 degrees of freedom
## Multiple R-squared:  0.9925, Adjusted R-squared:  0.9924
## F-statistic:  6522 on 3 and 147 DF,  p-value: < 2.2e-16
```

f. What is the mean sepal length for the species setosa?

5.0060

g. What is the mean sepal length for the species versicolor?

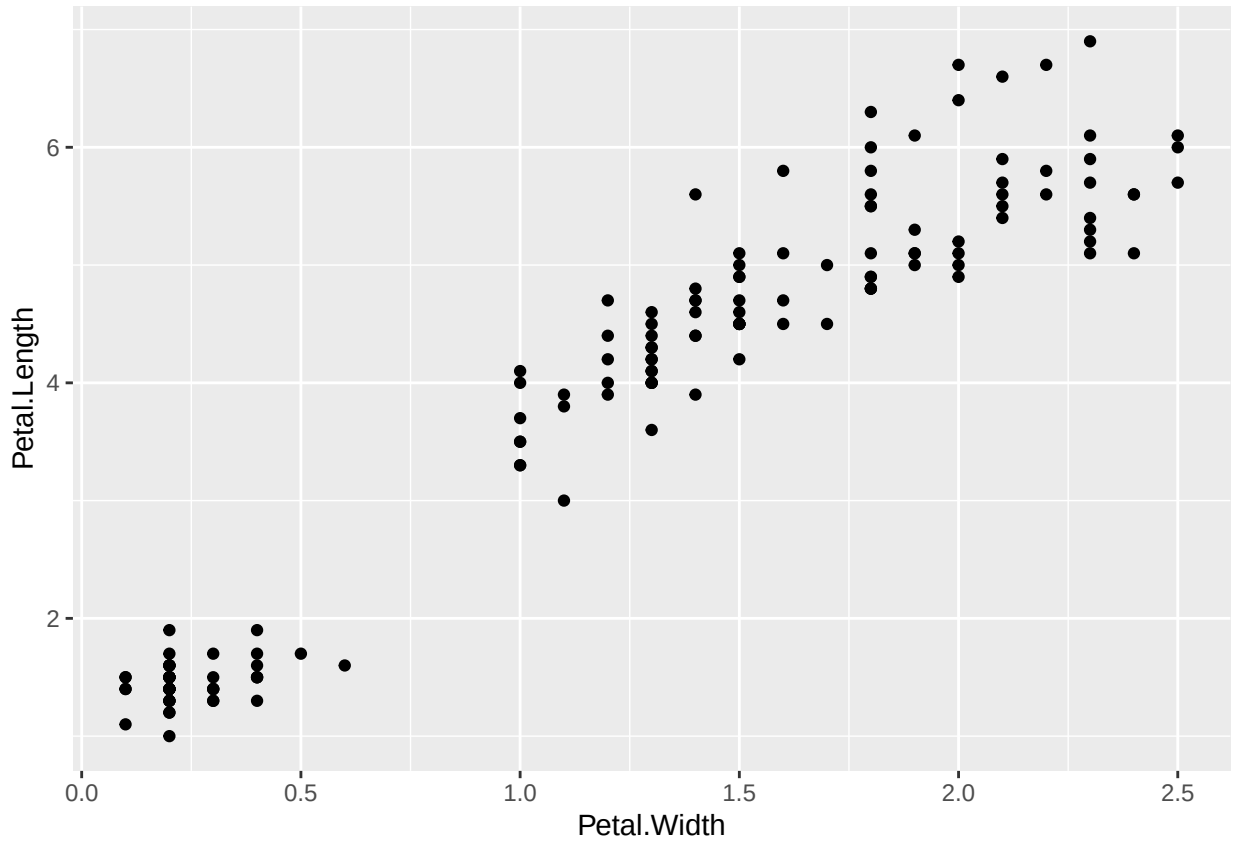
5.9360

Problem 3: Regression

Can we describe the relationship between petal length and petal width?

a. Create a scatterplot with petal length on the y-axis and petal width on the x-axis using ggplot.

```
ggplot(data=iris, aes(x=Petal.Width, y=Petal.Length)) +
  geom_point()
```



b. Create a linear model to model petal length with petal width (length is the response variable and width is the explanatory variable) using lm.

```
petal.model <- lm(data=iris, Petal.Length ~ Petal.Width)
summary(petal.model)
```

```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width, data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.33542 -0.30347 -0.02955  0.25776  1.39453
##
## Coefficients:
```

```
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.08356    0.07297   14.85   <2e-16 ***
## Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4782 on 148 degrees of freedom
## Multiple R-squared:  0.9271, Adjusted R-squared:  0.9266
## F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e-16
```

c. What is the estimate of the slope parameter?

2.22994

d. What is the estimate of the intercept parameter?

1.08356

e. Use summary() to get additional information.

```
summary(petal.model)
```

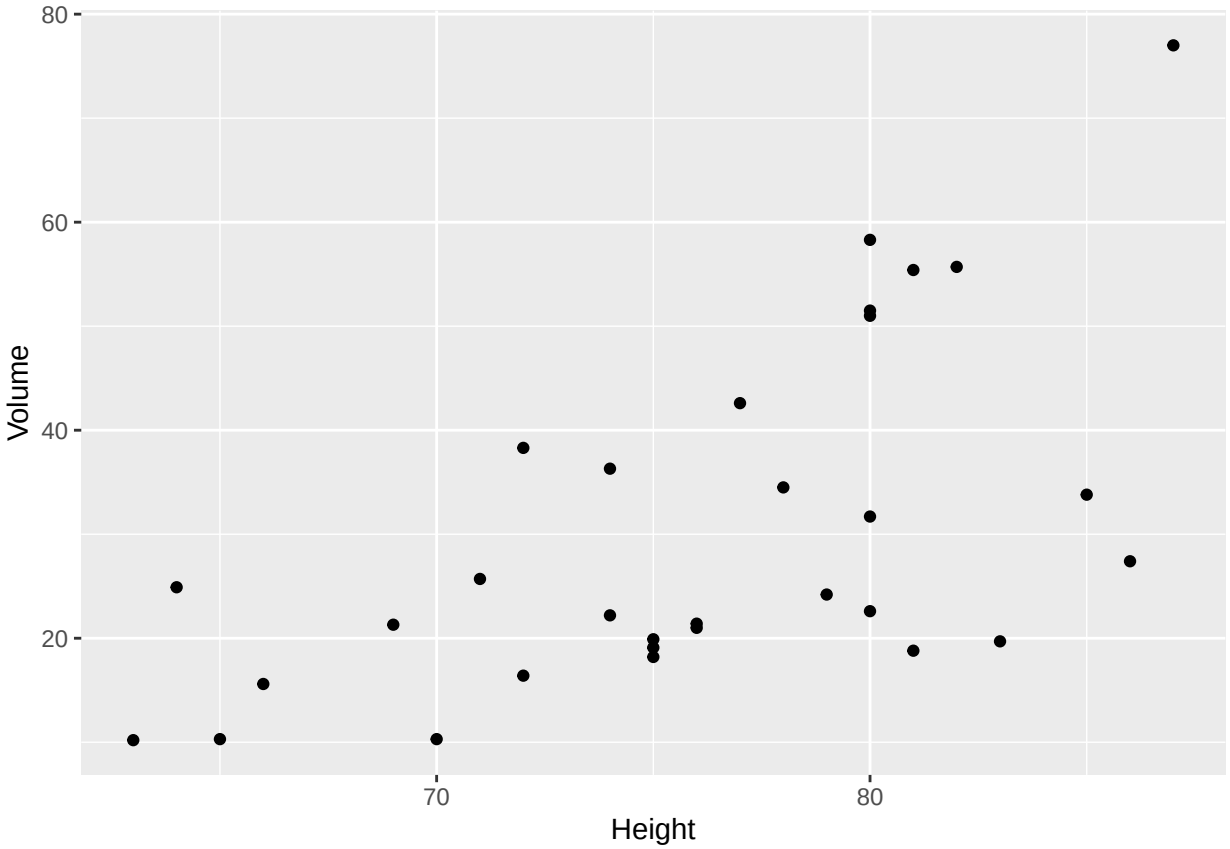
```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width, data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.33542 -0.30347 -0.02955  0.25776  1.39453
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.08356    0.07297   14.85   <2e-16 ***
## Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4782 on 148 degrees of freedom
## Multiple R-squared:  0.9271, Adjusted R-squared:  0.9266
## F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e-16
```

Problem 4: Modeling Trees

Using the `trees` data frame that comes pre-installed in R, follow the steps below to fit the regression model that uses the tree `Height` to explain the `Volume` of wood harvested from the tree.

a. Create a scatterplot of the data using ggplot.

```
ggplot(data=trees, aes(x=Height, y=Volume)) +
  geom_point()
```



b. Fit a `lm` model using the command `model <- lm(Volume ~ Height, data=trees)`.

```
model <- lm(Volume ~ Height, data=trees)
```

c. Print out the table of coefficients with estimate names, estimated value, standard error, and upper and lower 95% confidence intervals.

```
summary(model)
```

```
##
## Call:
## lm(formula = Volume ~ Height, data = trees)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -21.274  -9.894  -2.894  12.068  29.852
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -87.1236    29.2731  -2.976 0.005835 **
## Height        1.5433     0.3839   4.021 0.000378 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 13.4 on 29 degrees of freedom
## Multiple R-squared:  0.3579, Adjusted R-squared:  0.3358
## F-statistic: 16.16 on 1 and 29 DF,  p-value: 0.0003784
```

d.Add the model fitted values to the `trees` data frame along with the regression model confidence intervals. Note: the book does this in a super convoluted way. Don't follow the model in the book. Instead try cbind.

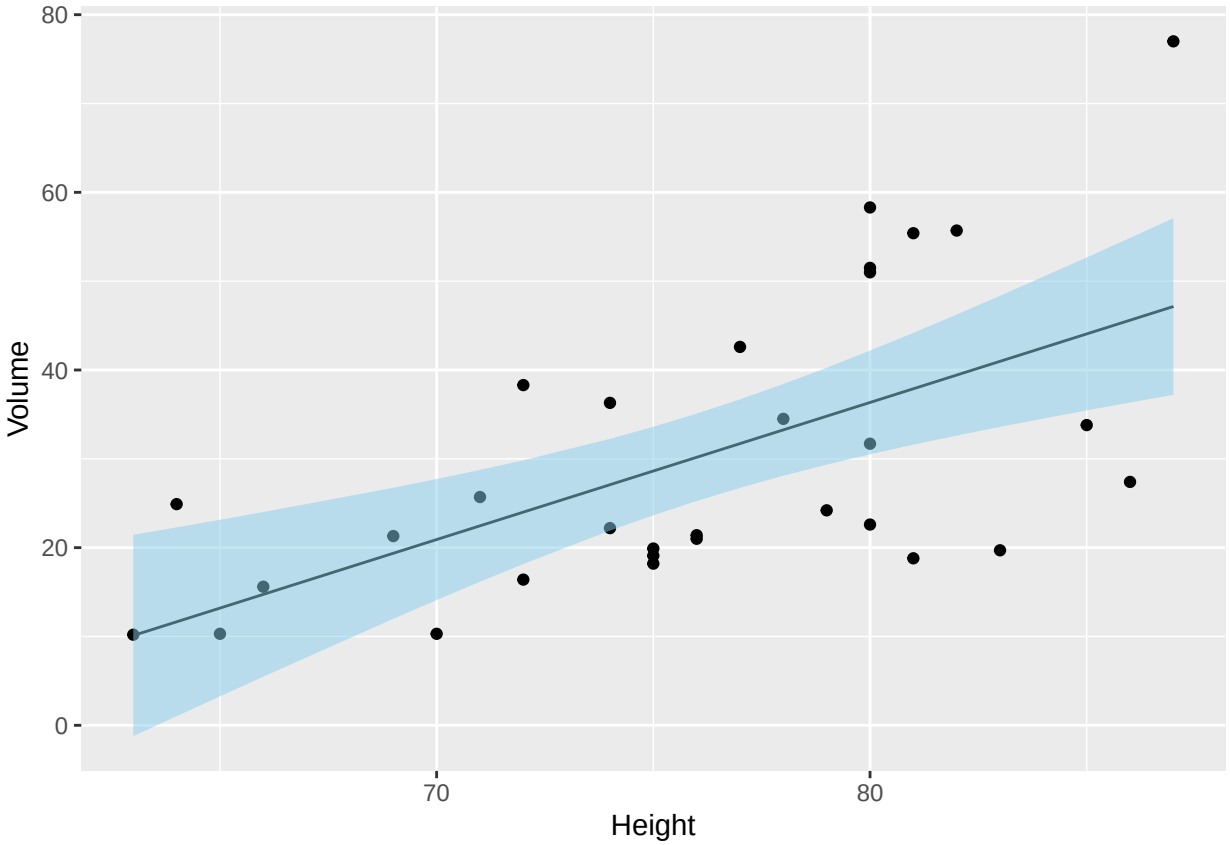
```
predict.model <- cbind(trees, predict(model, interval = "confidence"))

predict.model
```

```
##    Girth Height Volume      fit       lwr      upr
## 1    8.3     70   10.3 20.91087 14.098550 27.72319
## 2    8.6     65   10.3 13.19412  3.254288 23.13395
## 3    8.8     63   10.2 10.10742 -1.223363 21.43821
## 4   10.5     72   16.4 23.99757 18.159758 29.83538
## 5   10.7     81   18.8 37.88772 31.592680 44.18275
## 6   10.8     83   19.7 40.97442 33.597379 48.35145
## 7   11.0     66   15.6 14.73747  5.471607 24.00333
## 8   11.0     75   18.2 28.62762 23.644217 33.61102
## 9   11.1     80   22.6 36.34437 30.506556 42.18218
## 10  11.2     75   19.9 28.62762 23.644217 33.61102
## 11  11.3     79   24.2 34.80102 29.345254 40.25678
## 12  11.4     76   21.0 30.17097 25.249799 35.09214
## 13  11.4     76   21.4 30.17097 25.249799 35.09214
## 14  11.7     69   21.3 19.36752 11.990482 26.74456
## 15  12.0     75   19.1 28.62762 23.644217 33.61102
## 16  12.9     74   22.2 27.08427 21.918668 32.24987
## 17  12.9     85   33.8 44.06112 35.450370 52.67186
## 18  13.3     86   27.4 45.60447 36.338602 54.87033
## 19  13.7     71   25.7 22.45422 16.159183 28.74926
## 20  13.8     64   24.9 11.65077  1.021703 22.27984
## 21  14.0     78   34.5 33.25767 28.092067 38.42327
## 22  14.2     80   31.7 36.34437 30.506556 42.18218
## 23  14.5     74   36.3 27.08427 21.918668 32.24987
## 24  16.0     72   38.3 23.99757 18.159758 29.83538
## 25  16.3     77   42.6 31.71432 26.730917 36.69772
## 26  17.3     81   55.4 37.88772 31.592680 44.18275
## 27  17.5     82   55.7 39.43107 32.618747 46.24339
## 28  17.9     80   58.3 36.34437 30.506556 42.18218
## 29  18.0     80   51.5 36.34437 30.506556 42.18218
## 30  18.0     80   51.0 36.34437 30.506556 42.18218
## 31  20.6     87   77.0 47.14782 37.207982 57.08765
```

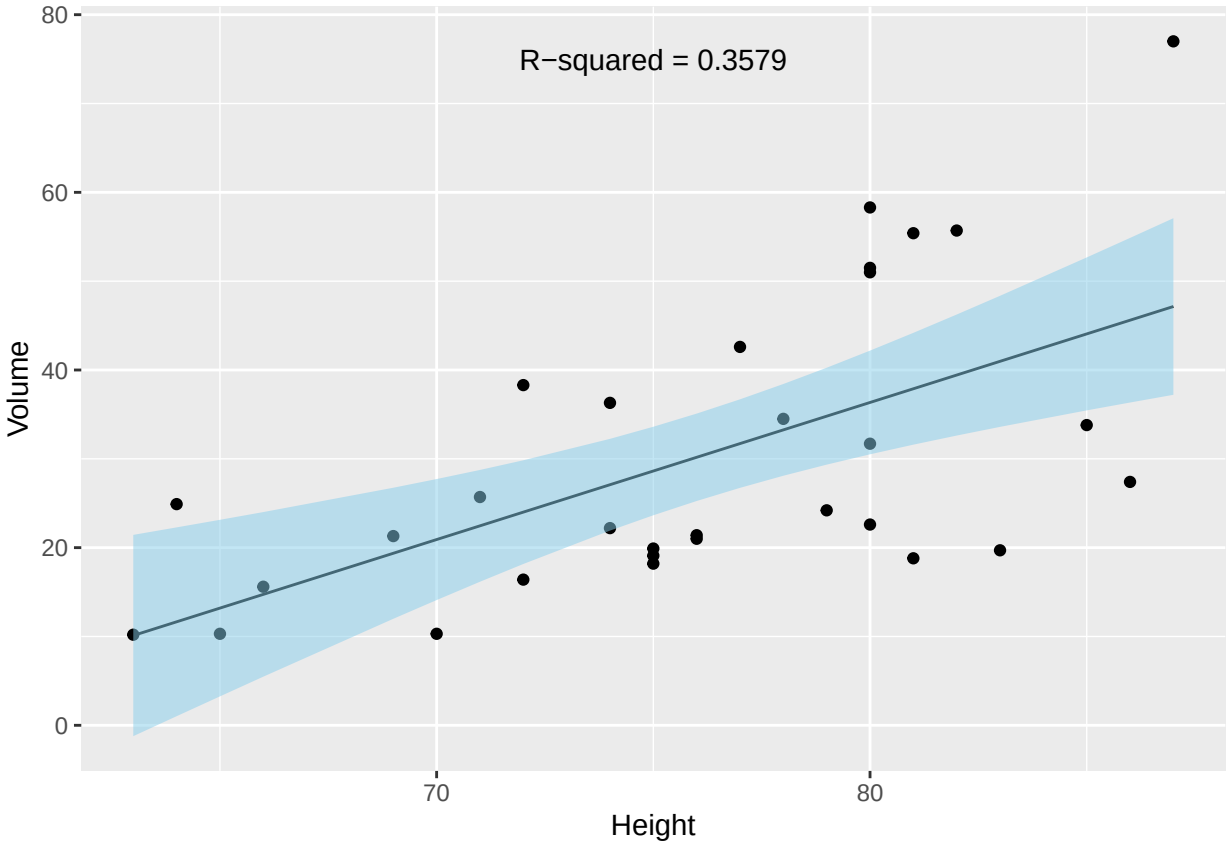
e. Graph the data and fitted regression line and uncertainty ribbon.

```
ggplot(data=predict.model, aes(x=Height, y=Volume)) +
  geom_point() +
  geom_line(aes(y=fit)) +
  geom_ribbon(aes(ymin=lwr, ymax=upr), alpha=0.5, fill="skyblue")
```



f. Add the R-squared value as an annotation to the graph using annotate.

```
ggplot(data=predict.model, aes(x=Height, y=Volume)) +
  geom_point() +
  geom_line(aes(y=fit)) +
  geom_ribbon(aes(ymin=lwr, ymax=upr), alpha=0.5, fill="skyblue") +
  annotate("text", x=75, y=75, label="R-squared = 0.3579")
```


R−squared = 0.3579
Volume
Height
80
60
40
20
0
70
80